Life History Traits and Genetic Diversity:

The Effects on He in Marine Species

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Hypothesis

Genetic diversity, especially in marine species, could be the result of various factors. From latitude/longitude to body length to reproduction strategies could cause either large or small genetic diversity in thousands of species. Despite the multitude of factors that could affect an outcome, the four traits that I want to focus on are body length, fertilization, reproduction mode, and fecundity of the species.

I am predicting that as body length increases, genetic diversity decreases. There seems to be a negative relationship between the two that studies have acknowledged as well (McCusker & Betzen, 2010). This relationship leads to the overarching idea of reproduction strategies in general. Body sizes are known to affect population size/fecundity as well. The pattern seen is large species have a much lower number of offspring compared to smaller species. One explanation is with survival, one that ties in with the idea of r- vs. k-strategies. Smaller spScecies tend to have much more offspring because of possible mortality rates due to predation or harsh environments (Winemiller & Rose 1993). Many studies also support the claim that a large population size leads to higher diversity, so the hypothesis of He increases w/ population size is valid (Harrang et al. 2013).

Fertilization and reproduction also have a close relationship with each other, as well as body length and fecundity. I predict that the external fertilization method would yield higher genetic diversity. Because fertilization ties in with body length and fecundity, there is a higher fecundity with external fertilization than internal fertilization. External fertilization may yield higher genetic diversity based on the fact that there can be multiple males. By having many offspring fertilized by multiples males, there can be higher genetic diversity. This diversity can lead to a higher survival rate and decreasing competition for resources (McLeod & Marshall 2009). It’s harder to see the significances resulting in diversity from internal fertilization species, but one can assume that the genetic diversity in external fertilization species would be higher.

I mentioned before fecundity and fertilization separately. However, these also have a relationship that can affect genetic diversity, as well. Having a large population that was fertilized by many males can increase genetic diversity. In smaller populations, there may be lower diversity, creating a bottleneck. Lower-diversity populations would also strive just to have smaller populations to keep competition for resources on a lower side, creating a cycle of smaller population 🡪 lower diversity 🡪 smaller population, and on (Johnson, Freiwald, & Bernardi 2016).

I also predict that hermaphroditic species (protogyny, protandry, or true hermaphroditism) would also have offspring with higher genetic diversity. The belief is that, by being hermaphroditic, the chances of reproduction can increase. There is no limitation on the sex of the fish that is around. For example, if the present circumstances require a female fish, then the fish can change into a female and allow for fertilization by present male fish. By adapting to the conditions, the individuals and species as a whole have more opportunities to reproduce. The need for adaption is present in clownfish. If the female dies, a male will change and take over as the female. These environmental factors, as well as genetics, allow for more offspring, leading to higher genetic diversity (Kobayashi et al. 2018).

However, these results may vary due to the molecular markers used in both microsatellites and mitochondrial DNA. Fecundity may not affect genetic diversity (Bazin, Glémin, & Galtier, 2006). Because of these, possible other factors may not also reflect more genetic diversity, such as fertilization strategies.  Also, there seem to be differences in results when it comes to comparing nucleotide diversity and microsatellite heterozygosity. Although there are still positive correlations with population and genetic diversity, the variation differs significantly from nucleotide diversity and microsatellites (Väli et al. 2008). Another study also concluded that there could be many reasons that mitochondrial DNA data may not work. Due to parasites that specifically target the mitochondria, the genetic diversity data collected may not reflect the individual's actual genetic diversity. Data collected can say there's less genetic variety, but parasites may have disrupted that. These factors must be acknowledged during the analysis and data collection.

Methods & Data Collection

I received select data of marine fish species for both microsatellites and mitochondrial DNA collections. Using this information, I wrote a R script that pulled data from Fishbase. I pulled data for the following traits: max length, mortality (wild), fecundity, fecundity mean, maturity length, maturity length mean, maturity age, maturity age mean, spawning cycles, reproductive season length (had to be recorded manually as it did not translate as nicely from Fishbase), fertilization, reproduction mode, spawning ground, whether the species are batch spawners, parental care, larvae size, and larvae size mean. This information was pulled for both microsatellites and mitochondrial DNA. However, the microsatellite and mitochondrial DNA data were not merged at this point.

After receiving the full data csv’s for marine species, both with microsatellite and mitochondrial DNA data, I went and merged my mitochondrial DNA data with the full mitochondrial DNA dataset together, repeating this process with microsatellites. From there, I focused on four specific traits: fertilization, reproduction mode, max length, and fecundity mean. I wrote a R script that analyzed the data against He (genetic diversity), plotting them in the respective plots. For fertilization, reproduction mode, and a more specific reproduction mode, box plots were required. For max length (with and without the Rhincodon Typus secies) and fecundity mean, scatter plots were required. I also created density plots for max length (w/ Rhincodon Typus) and fecundity mean. I performed T-tests on fertilization and reproduction mode, an Anova test for specific reproduction modes, and Wilcoxon tests for max length (w/ Rhincodon Typus) and fecundity mean. Because the mtDNA data was analyzed separately from msat data, at the end of my script, I compared all the plots previously created together, combining them so it is easier to understand. An important note to keep in mind is that there is much more microsatellite data than mitochondrial DNA data which may influence results and conclusions.

Results from Analysis

Running the R scripts allowed me to collect the data I was looking for. The first graph I obtained was a boxplot showing the relationship between fertilization methods and He. The plot seems to support my hypothesis that external fertilization leads to more genetic diversity. It is more noticeable with the mtDNA data as the mean for external fertilization is much higher than internal fertilization. For the microsatellite data, the means look much closer. However, external fertilization still seems to yield more genetic variation than internal fertilization. A screenshot of a cell phone

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For reproduction modes vs. He, I decided to create two separate graphs. The first graph would just focus on dioecious vs. hermaphroditic species. The plot supports the hypothesis that hermaphroditic species have genetic diversity than dioecious species. Again, it is more apparent with the mtDNA data, as the hermaphrodite mean is much higher. The means for microsatellite data is closer but hermaphrodites have a slightly higher mean. The second graph created separated hermaphrodites into the separate categories so it is easier to see the specific means for each type (protandry, protogyny, & true Hermaphroditism). The three different types of reproduction for hermaphrodites all have means that are larger than dioecious species. For microsatellite data, protandry and protogyny reproduction have relatively similar means with protandry resulting in a large He. This relationship varies from mtDNA data, which display protogyny reproduction with a higher He. It is important to note that for both markers, true hermaphroditism has the highest mean. This may because fewer species are true hermaphrodites, resulting in a smaller sample size that result in majority high He. A screenshot of a cell phone

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Next, I focused on max length which required a scatter plot. I had created two separate plots, one with Rhincodon Typus and one without for clarity. As expected, there was a negative correlation between length and expected heterozygosity. There seems to be a sharper decrease in the mitochondrial DNA data than the microsatellite data. Another thing to point out is that the microsatellite data seems to have no change in linear regression when the Rhincodon Typus data was removed. However, the mtDNA data changed, albeit by 0.01, when the Rhincodon Typus data was removed.  A screenshot of a cell phone

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**\*\*\*MIGHT REMOVE THE PLOT W/ NO R. TYPUS SINCE IT HAS NOT MUCH OF AN AFFECT. THE LOG TRANSFORMATION MADE IT EASIER TO SEE THE DATA WITHOUT EXCLUDING THE DATA\*\*\***

The last plot created illustrated the relationship between mean fecundity and He. It is important to note that out of all the data used for the previous plots, fecundity mean has the smallest recorded amount of data, which may or may not affect the final results. The scatter plot supports the hypothesis that a higher fecundity may lead to higher genetic diversity. Because mtDNA has less data, there seems to be a steeper increase in slope as opposed to the microsatellite data. Another important aspect to keep in mind is that the x axis went through a log transformation, which affected the data. A close up of a map

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